

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2003, 14:50:12 ; Search time 41 Seconds  
(without alignments)  
1951.129 Million cell updates/sec

Title: US-09-831-805A-6

Perfect score: 1635

Sequence: 1 MALRRPPLRLCARLPDFL.....VNYRTDEGDFRHKSFVI 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1629	99.6	310	4	Q9BX67
2	1629	99.6	355	4	Q8WML8
3	1620	99.1	309	4	Q96FL1
4	1417	86.7	310	11	Q9D8B7
5	1415	86.5	310	11	Q9EPK4
6	1403	85.8	310	11	Q9D1M9
7	481.5	29.4	298	11	Q9J159
8	481.5	29.4	298	11	Q8C5K9
9	478.5	29.3	298	11	Q8CE95
10	458.5	28.0	300	11	Q9JHV1
11	449.5	27.5	300	11	Q8VC39
12	331	20.2	259	4	Q9Y5B2
13	321	19.6	173	11	Q9JKD5
14	291	17.8	64	11	Q8BT59
15	248	15.2	318	13	Q91664
16	242.5	14.8	304	11	Q9CVA4

17	241	14.7	327	4	Q96IQ7
18	239.5	14.6	284	4	Q9NX42
19	239.5	14.6	325	4	Q95791
20	232.5	14.2	328	11	Q92109
21	221.5	13.5	319	11	Q922D5
22	215.5	13.2	319	11	Q9JKA5
23	215	13.1	407	11	Q9D2J4
24	209.5	12.8	335	13	Q9PWR4
25	209	12.8	181	13	Q91665
26	206.5	12.6	335	13	Q9YGH1
27	205.5	12.6	248	11	Q9D0T4
28	201.5	12.3	335	13	Q9YGV5
29	199.5	12.2	372	13	Q90150
30	197.5	12.1	373	4	Q9H6B4
31	193.5	11.8	795	13	Q90YMO
32	189	11.6	259	4	Q95532
33	187	11.4	725	13	Q73633
34	186.5	11.4	358	13	Q90490
35	184.5	11.3	838	13	Q90YML
36	182.5	11.2	372	11	Q8K1G0
37	182.5	11.2	1409	13	Q8J127
38	182.5	11.2	1428	13	Q8AY67
39	180.5	11.0	1894	11	Q64487
40	180	11.0	344	5	Q8WR42
41	180	11.0	345	5	Q8MPV0
42	180	11.0	435	5	Q8WR44
43	180	11.0	436	5	Q8MPV1
44	180	11.0	443	5	Q8WR43
45	180	11.0	444	5	Q8MPU9

#### ALIGNMENTS

RESULT 1

Q9BX67 PRELIMINARY; PRT; 310 AA.

AC Q9BX67; (Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Junctional adhesion molecule 3 precursor (Junctional adhesion molecule-2) (Junctional adhesion molecule-3) (Hypothetical protein FLJ90288) (Hypothetical protein FLJ90828).  
 GN JAM-2 OR JAM3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Cunningham S.A., Arrate M.P., Tran T.M.;  
 RT "Cloning of Human Junctional Adhesion Molecule 3.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Aurrand-Lions M.A., Johnson-leger C., Wong C., Dupasquier L.;  
 RT "Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM family members.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;  
 RT "Junctional adhesion molecules (JAMs) and interendothelial junctions.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Sachs U.J.H., Eva O., Berghoefer H., Santos S.;  
 RT "Characterization of Junctional Adhesion Molecule-3 on Human Platelets: A New Member of Immunoglobulin Superfamily.";

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RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Isoqai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.,
RT "NEDO human cDNA sequencing project.",
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF356518; AAK27221.1; -.
DR EMBL; AJ344431; AAC69845.1; -.
DR EMBL; AF448478; AAC20925.1; -.
DR EMBL; AK074769; BAC11195.1; -.
DR EMBL; AK075309; BAC11538.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS50835; IG LIKE; 2.
KW Hypothetical protein; Signal.
FT SIGNAL 1 30
SQ SEQUENCE 310 AA; 35020 MW; CE39ADF33BA1DAB9 CRC64;
    Query Match      99.6%; Score 1629; DB 4; Length 310;
    Best Local Similarity 99.7%; Pred. No. 2.2e-152;
    Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    QY 1 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSSNRTVPVQEFSEVLSCTIIDSQT 60
    DB 1 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSSNRTVPVQEFSEVLSCTIIDSQT 60
    QY 61 SDPIEWKKIQDEQTYVFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVVAR 120
    DB 61 SDPIEWKKIQDEQTYVFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVVAR 120
    QY 121 NDRKEIDEIVELTVQVKPVPVCRVPAVPVGMKATLHCQESGHPHYSWYRNDVPL 180
    DB 121 NDRKEIDEIVELTVQVKPVPVCRVPAVPVGMKATLHCQESGHPHYSWYRNDVPL 180
    QY 181 PTDSRANPRFRNSSSHLNSSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEVEVDL 240
    DB 181 PTDSRANPRFRNSSSHLNSSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEVEVDL 240
    QY 241 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKPKGPDGVNYIRTDDEG 300
    DB 241 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKPKGPDGVNYIRTDDEG 300
    QY 301 DFRHKSFPVI 310
    DB 301 DFRHKSFPVI 310
    RESULT 2
    Q8WL8 PRELIMINARY; PRT; 355 AA.
    AC Q8WL8;
    DT 01-MAR-2002 (TrEMBLrel. 20, Created)
    DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
    DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
    DE Junction adhesion molecule 3.
    GN JAM3.
    OS Homo sapiens (Human).
    OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    OX NCBI_TaxID=9606;
    RN [1]
    RP SEQUENCE FROM N.A.
    RA Hearn T.;
    RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
    RN [2]
    RP SEQUENCE FROM N.A.
    RA Phillips H.M.;
    RT "Narrowing the critical region within 11q24-qter for hypoplastic left
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RT heart and identification of a candidate gene, JAM3, expressed during
RL cardiogenesis.";
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416101; CAC94776.1; -.
DR Genew; HGNC:15532; JAM3.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain.
FT CHAIN 76 355
SQ SEQUENCE 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;
    Query Match      99.6%; Score 1629; DB 4; Length 355;
    Best Local Similarity 99.7%; Pred. No. 2.7e-152;
    Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    QY 1 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSSNRTVPVQEFSEVLSCTIIDSQT 60
    DB 46 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSSNRTVPVQEFSEVLSCTIIDSQT 105
    QY 61 SDPIEWKKIQDEQTYVFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVVAR 120
    DB 106 SDPIEWKKIQDEQTYVFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVVAR 165
    QY 121 NDRKEIDEIVELTVQVKPVPVCRVPAVPVGMKATLHCQESGHPHYSWYRNDVPL 180
    DB 166 NDRKEIDEIVELTVQVKPVPVCRVPAVPVGMKATLHCQESGHPHYSWYRNDVPL 225
    QY 181 PTDSRANPRFRNSSSHLNSSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEVEVDL 240
    DB 226 PTDSRANPRFRNSSSHLNSSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEVEVDL 285
    QY 241 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKPKGPDGVNYIRTDDEG 300
    DB 286 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKPKGPDGVNYIRTDDEG 345
    QY 301 DFRHKSFPVI 310
    DB 346 DFRHKSFPVI 355
    RESULT 3
    Q96FL1 PRELIMINARY; PRT; 309 AA.
    AC Q96FL1;
    DT 01-DEC-2001 (TrEMBLrel. 19, Created)
    DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
    DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
    DE Hypothetical protein (Fragment).
    OS Homo sapiens (Human).
    OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    OX NCBI_TaxID=9606;
    RN [1]
    RP SEQUENCE FROM N.A.
    RC TISSUE=Eye;
    RA Strausberg R.;
    RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
    DR EMBL; BC010690; AAH10690.1; -.
    DR InterPro; IPR007110; IG-like.
    DR InterPro; IPR003598; IG_C2.
    DR InterPro; IPR003006; IG_MHC.
    DR Pfam; PF00047; ig; 2.
    DR SMART; SM00408; IGC2; 1.
    DR PROSITE; PS50835; IG LIKE; 2.
    KW Hypothetical protein; Immunoglobulin domain.
    FT NON_TER 1
    SQ SEQUENCE 309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;
    Query Match      99.1%; Score 1620; DB 4; Length 309;
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Best Local Similarity 99.4%; Pred. No. 1.7e-151; Matches 307; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	2 ALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRPVVOEFESVELSCIITDSOTS 61
Db	1 ALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRPVVOEFESVELSCIITDSOTS 60
QY	62 DPRIEWKKIQDEQTTVVFDNKKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVARN 121
Db	61 DPRIEWKKIQDEQTTVVFDNKKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVARN 120
QY	122 DRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESGHPHYSWYRNDVPL 181
Db	121 DRKEIDEIVIELTVRVPKVPVCRVPKAVPVGKMATLHCQESGHPHYSWYRNDVPL 180
QY	182 TDSRANPRFNSSSHLSNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEMEYDIN 241
Db	181 TDSRANPRFNSSSHLSNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEMEYDIN 240
QY	242 IGGIIGVVLVLAVALITLIGICAYRRGYFINNKQDGESYKXNPKGPDGVNVRTDEGD 301
Db	241 IGGIIGVVLVLAVALITLIGICAYRRGYFINNKQDGESYKXNPKGPDGVNVRTDEGD 300
QY	302 FRHKSSEVI 310
Db	301 FRHKSSEVI 309
RESULT 4	
Q9DB87	PRELIMINARY; PRT; 310 AA.
AC	Q9DB87
DT	01-JUN-2001 (TReMBLrel. 17, Created)
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT	01-WAR-2003 (TReMBLrel. 23, Last annotation update)
DE	1110002N23Rik protein.
GN	JCAM3 OR JCAM2 OR 1110002N23RIK.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Small intestine;
RX	MEDLINE=21085660; PubMed=11217851;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA	Hayashizaki Y.
RA	"Functional annotation of a full-length mouse cDNA collection."
RL	Nature 409:685-690 (2001).
DR	EMBL; AK008187; BAB25519.1; -.
DR	MED; MGI:1933820; Jcam2.
DR	MED; MGI:1933825; Jcam3.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003598; IG_c2.
DR	InterPro; IPR003006; IG_MHC.
DR	Pfam; PF00047; IG; 2.
DR	SMART; SM00408; IGc2; 1.
Best Local Similarity 99.4%; Pred. No. 1.7e-151; Matches 307; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	2 ALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRPVVOEFESVELSCIITDSOTS 61
Db	1 ALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRPVVOEFESVELSCIITDSOTS 60
QY	62 DPRIEWKKIQDEQTTVVFDNKKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVARN 121
Db	61 DPRIEWKKIQDEQTTVVFDNKKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVARN 120
QY	122 DRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESGHPHYSWYRNDVPL 181
Db	121 DRKEIDEIVIELTVRVPKVPVCRVPKAVPVGKMATLHCQESGHPHYSWYRNDVPL 180
QY	182 TDSRANPRFNSSSHLSNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEMEYDIN 241
Db	181 TDSRANPRFNSSSHLSNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEMEYDIN 240
QY	242 IGGIIGVVLVLAVALITLIGICAYRRGYFINNKQDGESYKXNPKGPDGVNVRTDEGD 301
Db	241 IGGIIGVVLVLAVALITLIGICAYRRGYFINNKQDGESYKXNPKGPDGVNVRTDEGD 300
QY	302 FRHKSSEVI 310
Db	301 FRHKSSEVI 309
RESULT 5	
Q9EPK4	PRELIMINARY; PRT; 310 AA.
AC	Q9EPK4
DT	01-MAR-2001 (TReMBLrel. 16, Created)
DT	01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE	Functional adhesion molecule-2, JAM-2 (1110002N23Rik protein)
DE	(Junction cell adhesion molecule 3).
GN	JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Embryo;
RX	MEDLINE=21085660; PubMed=11217851;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA	Hayashizaki Y.
RA	"Functional annotation of a full-length mouse cDNA collection."
RL	Nature 409:685-690 (2001).
DR	EMBL; AK008187; BAB25519.1; -.
DR	MED; MGI:1933820; Jcam2.
DR	MED; MGI:1933825; Jcam3.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003598; IG_c2.
DR	InterPro; IPR003006; IG_MHC.
DR	Pfam; PF00047; IG; 2.
DR	SMART; SM00408; IGc2; 1.
Best Local Similarity 99.4%; Pred. No. 1.7e-151; Matches 307; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	2 ALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRPVVOEFESVELSCIITDSOTS 61
Db	1 ALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRPVVOEFESVELSCIITDSOTS 60
QY	62 DPRIEWKKIQDEQTTVVFDNKKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVARN 121
Db	61 DPRIEWKKIQDEQTTVVFDNKKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVARN 120
QY	122 DRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESGHPHYSWYRNDVPL 181
Db	121 DRKEIDEIVIELTVRVPKVPVCRVPKAVPVGKMATLHCQESGHPHYSWYRNDVPL 180
QY	182 TDSRANPRFNSSSHLSNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEMEYDIN 241
Db	181 TDSRANPRFNSSSHLSNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEMEYDIN 240
QY	242 IGGIIGVVLVLAVALITLIGICAYRRGYFINNKQDGESYKXNPKGPDGVNVRTDEGD 301
Db	241 IGGIIGVVLVLAVALITLIGICAYRRGYFINNKQDGESYKXNPKGPDGVNVRTDEGD 300
QY	302 FRHKSSEVI 310
Db	301 FRHKSSEVI 309
RESULT 6	
Q9EPK4	PRELIMINARY; PRT; 310 AA.
AC	Q9EPK4
DT	01-MAR-2001 (TReMBLrel. 16, Created)
DT	01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE	Functional adhesion molecule-2, JAM-2 (1110002N23Rik protein)
DE	(Junction cell adhesion molecule 3).
GN	JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Embryo;
RX	MEDLINE=21085660; PubMed=11217851;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA	Hayashizaki Y.
RA	"Functional annotation of a full-length mouse cDNA collection."
RL	Nature 409:685-690 (2001).
DR	EMBL; AK008187; BAB25519.1; -.
DR	MED; MGI:1933820; Jcam2.
DR	MED; MGI:1933825; Jcam3.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003598; IG_c2.
DR	InterPro; IPR003006; IG_MHC.
DR	Pfam; PF00047; IG; 2.
DR	SMART; SM00408; IGc2; 1.

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;  
RX MEDLINE=22354683; PubMed=12466851;  
RA Straussberg R.;  
RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RL the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; AJ300304; CAC20704.1; -;  
DR EMBL; AK013156; BAB28683.1; -;  
DR EMBL; BC024357; BAH24357.1; -;  
DR EMBL; AK032833; BAC28049.1; -;  
DR MGD; MGI:1933820; Jcam2.  
DR MGD; MGI:1933825; Jcam3.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; ig; 2.  
DR SMART; SM00408; Igc2; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
KW Immunoglobulin domain.  
SQ SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;  
  
Query Match 86.5%; Score 1415; DB 11; Length 310;  
Best Local Similarity 86.1%; Pred. No. 3.1e-131;  
Matches 267; Conservative 18; Mismatches 25; Indels 0; Gaps 0;  
  
QY 1 MALRPPRLRLCARLPDFFLLFRGLGAVNLKSSNRTPVVQGFESVELSCIITDSQT 60  
DB 1 MALSRLRLRLYARLPDFFLLFRGCMIEAVNLKSSNRPVHFEFVELSCIITDSQT 60  
  
QY 61 SDPIEWKKIQDEQTTVYFDNKKIQGLAGRAEILGKTSKIWNVTRRDSALYRCEVVAR 120  
DB 61 SDPIEWKKIQDQTTVYFDNKKIQGLAGRTDVFGRKSLRWNVTRSDSALYRCEVVAL 120  
  
QY 121 NDRKEIDEIVELTVQVKPVPVCRPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180  
DB 121 NDRKEVDEITIELIVQVKPVPVCRIPAAVPVGKATLQCQSEGYPRPHYSWYRNDVPL 180  
  
QY 181 PTDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEVEYDL 240  
DB 181 PTDSRANPRFQNSFHVNSEITGLVFNHVKDDSGQYCIASNDAGARCEQDMEYDL 240  
  
QY 241 NIGGIIGVVLVAVLALITLIGICAYRRGYFINNKQDGESYKPNKPGKPDGVNYIRTDSEEG 300  
DB 241 NIAGIIGVVLVAVLAVITMGICCAVRRGCFISSKQDGESYKSPGKHGQVNYIRTDSEEG 300  
  
QY 301 DFRHKSFFVI 310  
DB 301 DFRHKSFFVI 310  
  
RESULT 6  
Q9D1M9 ID Q9D1M9 PRELIMINARY; PRT; 310 AA.  
AC Q9D1M9;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE 1110002N23rik protein.  
GN JCAM3 OR JCAM2 OR 1110002N23RIK.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL; AK003326; BAB22715.1; -;  
DR MGD; MGI:1933820; Jcam2.  
DR MGD; MGI:1933825; Jcam3.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; ig; 2.  
DR SMART; SM00408; Igc2; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
KW Immunoglobulin domain.  
SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;  
  
Query Match 85.8%; Score 1403; DB 11; Length 310;  
Best Local Similarity 85.2%; Pred. No. 4.7e-130;  
Matches 264; Conservative 20; Mismatches 26; Indels 0; Gaps 0;  
  
QY 1 MALRPPRLRLCARLPDFFLLFRGLGAVNLKSSNRTPVVQGFESVELSCIITDSQT 60  
DB 1 MALSRLRLRLYARLPDFFLLFRGCMIEAVNLKSSNRPVHFEFVELSCIITDSQT 60  
  
QY 61 SDPIEWKKIQDEQTTVYFDNKKIQGLAGRAEILGKTSKIWNVTRRDSALYRCEVVAR 120  
DB 61 SDPIEWKKIQDQTTVYFDNKKIQGLAGRTDVFGRKSLRWNVTRSDSALYRCEVVAL 120  
  
QY 121 NDRKEIDEIVELTVQVKPVPVCRPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180  
DB 121 NDRKEVDEITIELIVQVKPVPVCRIPAAVPVGKATLQCQSEGYPRPHYSWYRNDVPL 180  
  
QY 181 PTDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEVEYDL 240  
DB 181 PTDSRANPRFQNSFHVNSEITGLVFNHVKDDSGQYCIASNDAGARCEQDMEYDL 240  
  
QY 241 NIGGIIGVVLVAVLALITLIGICAYRRGYFINNKQDGESYKPNKPGKPDGVNYIRTDSEEG 300  
DB 241 NIAGIIGVVLVAVLAVITMGICCAVRRGCFISSKQDGESYKSPGKHGQVNYIRTDSEEG 300  
  
QY 301 DFRHKSFFVI 310  
DB 301 DFRHKSFFVI 310  
  
RESULT 7  
Q9J159 ID Q9J159 PRELIMINARY; PRT; 298 AA.  
AC Q9J159;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vascular endothelial junction-associated molecule (Junctional adhesion
DE molecule-3) (2410030G2RIK protein)
GN JCAM3 OR JCAM2 OR JAM-3 OR 2410030G2RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20317114; PubMed=10779521;
RA Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
RA "Vascular Endothelial Junction-associated Molecule, a Novel Member of
RT the Immunoglobulin Superfamily, Is Localized to Intercellular
RT Boundaries of Endothelial Cells.";
RL J. Biol. Chem. 275:19139-19145(2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX PubMed=11036763;
RA Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT Family";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saio T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AF255911; AAF81224.1; -
DR EMBL; AJ291757; CAC20699.1; -
DR EMBL; AK013914; BAB29053.1; -
DR EMBL; AK010616; BAB27064.1; -
DR MGD; MGI:1933820; Jcam2.
DR MGD; MGI:1933825; Jcam3.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 33047 MW; 1124E0F07B6CF751 CRC64;

Query Match 29.4%; Score 481.5; DB 11; Length 298;
Best Local Similarity 36.7%; Pred. No. 4.7e-39;
Matches 114; Conservative 53; Mismatches 11; Indels 27; Gaps 9;

QY 13 ARLPDFFLLPRGLGICAVNLKSN-----RTPVQEFESVELSCIITDSQTSDP 63
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 RIEWKKIQDEQTYVFFDNKIQDGLAGRAELIGKTSIKWNVTRRDSALYRCVVARNDR 123
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RLEWKV-QGGVSLVYQQALQGFQKRAEMI-DENIRIKNVTSDAGEYRCVSAPTAQ 118
QY 124 -KEIDEIVIELTVQKPTVPCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPT 182
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 119 GONLQEDKWLVLVAPAVPACVPTSVMTGVSVELRCQDKEGNPAPEYIWFKDGSL-- 176
QY 183 DSRANPRF---NSSSHLNSETGLVFTAVHKDSDGQYCIASNDAGSARCEQEYVD 239
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 177 --LGNPKGRTHNNSYTMNTKSGILQFNIMISKDMSGEYICARNVSGHRRCPGKRMQYDV 234
QY 240 LNIIGIIGGVLLVAVLALITLIGCCAVRRGYFINNKDGESYKNGPKPGDGVNVRTDEE 299
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 GDFRHKSFFVI 310
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 288 NDFKHTKSFII 298

RESULT 9
Q8CE95 PRELIMINARY; PRT; 298 AA.
ID Q8CE95

Query Match 29.4%; Score 481.5; DB 11; Length 298;
Best Local Similarity 36.7%; Pred. No. 4.7e-39;
Matches 115; Conservative 53; Mismatches 116; Indels 27; Gaps 9;

QY 13 ARLPDFFLLPRGLGICAVNLKSN-----RTPVQEFESVELSCIITDSQTSDP 63
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 RIEWKKIQDEQTYVFFDNKIQDGLAGRAELIGKTSIKWNVTRRDSALYRCVVARNDR 123
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RLEWKV-QGGVSLVYQQALQGFQKRAEMI-DENIRIKNVTSDAGEYRCVSAPTAQ 118
QY 124 -KEIDEIVIELTVQKPTVPCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPT 182
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 119 GONLQEDKWLVLVAPAVPACVPTSVMTGVSVELRCQDKEGNPAPEYIWFKDGSL-- 176
QY 183 DSRANPRF---NSSSHLNSETGLVFTAVHKDSDGQYCIASNDAGSARCEQEYVD 239
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 177 --LGNPKGRTHNNSYTMNTKSGILQFNIMISKDMSGEYICARNVSGHRRCPGKRMQYDV 234
QY 240 LNIIGIIGGVLLVAVLALITLIGCCAVRRGYFINNKDGESYKNGPKPGDGVNVRTDEE 299
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 GDFRHKSFFVI 310
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 288 NDFKHTKSFII 298

RESULT 9
Q8CE95 PRELIMINARY; PRT; 298 AA.
ID Q8CE95
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QY 75 TTYVFFDNKIQDLAGRAEILGKTSKINWVTRRDSALYRCVAVARNDRKEIDEIVIELT 134
Db 69 TALVCYNSQITAPYADRV-TFSSGITFSSVTRKONGEYTC-MVSEGGQNYGEVSIHLT 126
QY 135 VOVKPVTPVCRVPKAVPGKMATLHCQSEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
Db 127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDSPPSEYFNGKDGISMLTADAKKTRAFMNS 186
QY 194 SSSLNSETGLTFTAVHKDDSQYCYCIASNDAGSA-RCEQEEMEVYDNLNIGIIGVLV 252
Db 187 SFTIDPKSGDLIFDFTAFDSEYVCOAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246
QY 253 LAVLATILGICCAVRGYFINNKGDSYKPNKPGDGVNVRTDEEGDPRHKSFSVI 310
Db 247 LILLGLLIFGVWFAYSRGVFERTKKG----TAPGKKVIYQSPSTRSEGEFKQTSFLV 300

RESULT 12
QY5B2
ID QY5B2 PRELIMINARY; PRT; 259 AA.
AC QY5B2;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Junctional adhesion molecule.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Liu Y., Nusrat A., Schnell F.J., Walsh S., Reeves T.A., Pochet M.,
RA Foley C., Parkos C.A.;
RT "Human junctional adhesion molecule is expressed by polarized columnar
RT epithelia and regulates tight junction resealing.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154005; AAD43794.1; -.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG_2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 259 AA; 28122 MW; FE38521A911582D0 CRC64;

Query Match 20.2%; Score 331; DB 4; Length 259;
Best Local Similarity 29.6%; Pred. No. 2.9e-24;
Matches 81; Conservative 44; Mismatches 111; Indels 38; Gaps 7;

QY 42 VQVPESEVELCIITDSQTSQPIBWKIODEQTYVFFDNKIQDLAGRAEILGKTSLK 101
Db 19 ILPENNPVKLSQAY--SGFSGPR---AASDYEDRVTL-----PTGIT 55

QY 102 IWNVTRRDSALYRCVAVARNDRKEIDEIVIELTVQKVPVCRVPKAVPGKMATLHCQ 161
Db 56 FKSVRTETGIYTC-MVPEEGNSGVEVKVLIIVLPSPKPTVINIPSSATIGNRAVLTC 114

QY 162 ESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSLNSETGLTFTAVHKDDSQYCYCIA 221
Db 115 EQDGSPPEYTWFKDGIWMPNPKSTRAFNSSYVNLNPTTGLVFDPLSADTGEYSCEA 174

QY 222 SNDAGSARCEQ-EDEVYDNLNIGIIGVLVLAVALITILGICCAVRGYFINNKGDS 280
Db 175 RNVGVTPTWTSNAVRMEARNVGVVAAVLVLAVALITILGILVFGVWFAYSRGVFERTK 234

QY 281 S----YKNPGKPGDGVNVRTDEEGDPRHKSFSVI 310
Db 235 SKKVIYQSPS-----ARSEGEFKQTSFLV 259

RESULT 13
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QY5B2
ID QY5B2 PRELIMINARY; PRT; 173 AA.
AC QY5B2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Junctional adhesion molecule (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RA Kirsch T., Wellner M., Haller H., Lippoldt A.;
RT "Cloning of the rat junctional adhesion molecule (JAM).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241261; AAF61729.1; -.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG_1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 1
SQ SEQUENCE 173 AA; 18706 MW; 3EE3ECDFA5AFB8B2 CRC64;

Query Match 19.6%; Score 321; DB 11; Length 173;
Best Local Similarity 40.3%; Pred. No. 1.6e-23;
Matches 71; Conservative 27; Mismatches 72; Indels 6; Gaps 3;

QY 137 VKPVPVCRVPKAVPGKMATLHCQSEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 195
Db 2 VPPSKPTVSPSSVTIGNRAVLTCSEHDSPPSEYFNGKDGVPMLTADAKKTRAFINSSY 61

QY 196 HLNSETGLTFTAVHKDDSQYCYCIASNDAGSA-RCEQEEMEVYDNLNIGIIGVLVLA 254
Db 62 TIDPKSGDLVFDPVSAFDSGEYCEAQNGYGTAMRSEAVRMEAVELNVGGIVAAVLTLI 121

QY 255 VLALITILGICCAVRGYFINNKGDSYKPNKPGDGVNVRTDEEGDPRHKSFSVI 310
Db 122 LLGLLIFGVWFAYSRGVFERTKKG----TAPGKKVIYQSPSARSEGEFKQTSFLV 173

RESULT 14
QY5B2
ID QY5B2 PRELIMINARY; PRT; 64 AA.
AC QY5B2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Junction cell adhesion molecule 3 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK017692; BAC25526.1; -.
FT NON TER 1
SQ SEQUENCE 64 AA; 6996 MW; AF46BC30AA6D0C11 CRC64;

Query Match 17.8%; Score 291; DB 11; Length 64;
Best Local Similarity 85.9%; Pred. No. 3.8e-21;
Matches 55; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
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